

1 agggagaggc agtgaaccatg aaggctgtgc tgcctgccct gtgtaggca  
51 ggcttggccc tgcagccagg cactgccctg ctgtgctact cctgcaaagc  
101 ccaggtgagc aacgaggact gccctgcaggt ggagaactgc acccagctgg  
151 gggagcagtg ctggaccgcg cgcatccgcg cagtggcct cctgaccgic  
201 arcagcaaag gctgcagctt gaactgcgtg gatgactcac aggactacta  
251 cgtgggcaag aagaacatca cgtgctgtga caccgacttg tgcaacgcc  
301 gcgggggccc tgccctgcag ccggctgccg ccatcctgc gctgctccct  
351 gcactcggcc tgcctgctctg gggacccggc cagctatagg ctctgggggg  
401 ccccgctgca gccacactg ggtgtggtgc ccagggcctt tgtgccactc  
451 ctacagaac ctggcccagt gggagcctgt cctggctcct gaggcacatc  
501 ctaacgcaag ttgaccaatg tatgtttgca cccctttcc cnaaccctg  
551 acctcccat gggcctttc caggattccn accnnggcaga tcagtittag  
601 tganacanat ccgctgtcag atggccctc caaccntttt tgttgntgtt  
651 tccatggccc agcattttc acccttaacc ctgtgttcag gcacttttc  
701 cccaggaag cctccctgc ccaccccat tatgaattga gccaggttg  
751 gtccgtggtg tccccgcac ccagcagggg acaggcaatc aggagggccc  
801 agtaagggt gagatgaagt ggactgagta gaactggagg acaagagtg  
851 acgtgagtc ctgggagtt ccagagatgg ggcctggagg cctggaggaa  
901 ggggccaggc ctacattg tggggtccc gaatggcagc ctgagcacag  
951 cgtaggccct taataaacac ctgtggata agccaaaaaa aaaaaaaa

MKAVLLALLMAGLALQPGTALLCYSCKAQVS NEDCLQV  
 ENCTQLGEQCWTARIRAVGLLTVISKGCSLNCVDDS  
 QDYYVGKKNITCCDIDLNASGAHALQPAAAILALLPAL  
 GLLLWGPGQL

Figure 1B

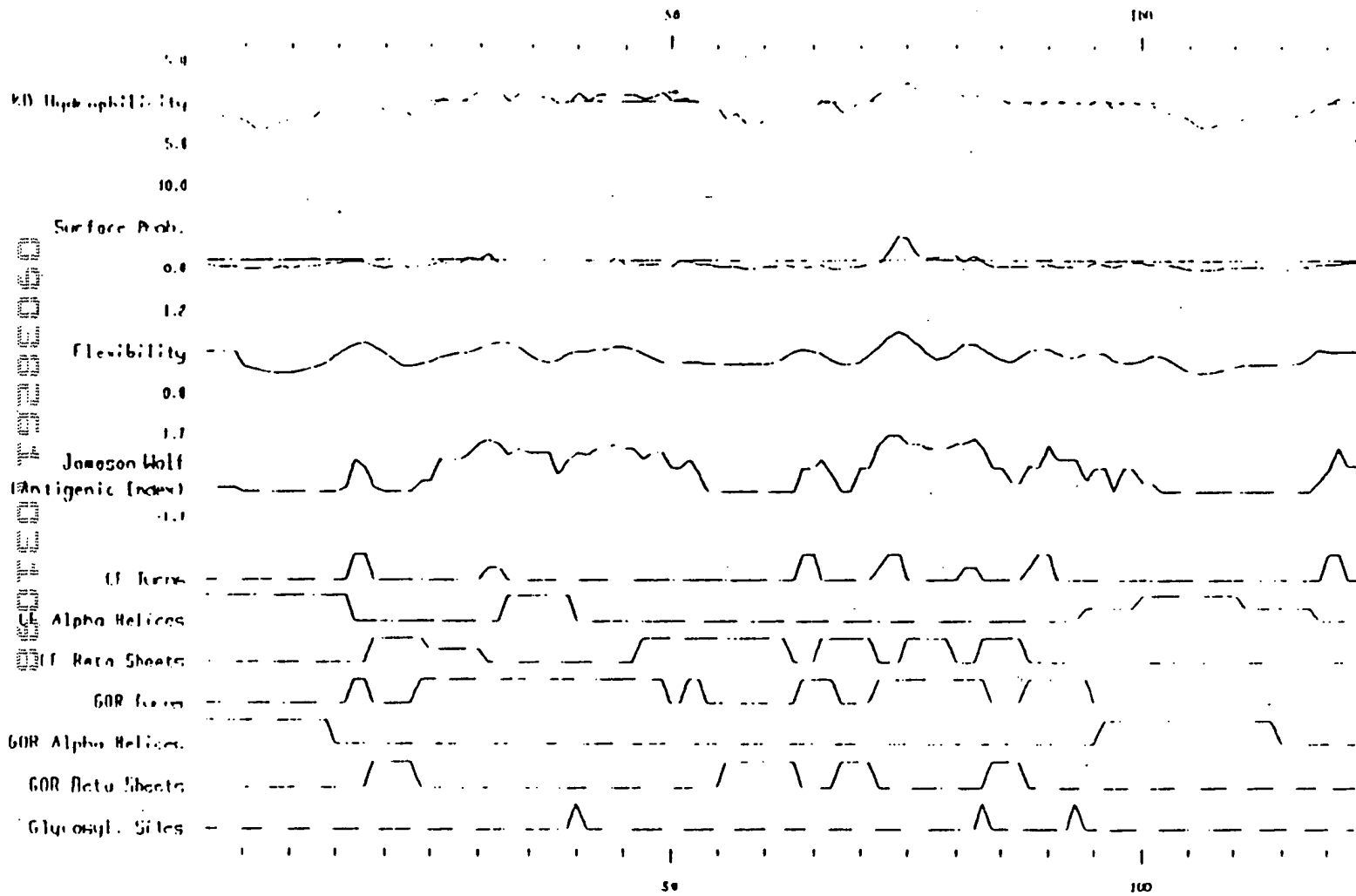
ATGAAGACAGTTTTTTTTTATCCTGCTGGCCACCTACTTAGCCCTGCATCCAGGTGCTGCT  
1 -----+-----+-----+-----+-----+-----+-----+ 60  
TACTTCTGTCAAAAAAATAGGACGACCGGTGGATGAATCGGGACGTAGGTCCACGACGA  
M K T V F F I L L A T Y L A L H P G A A -  
CTGCAGTGCTATTTCATGCACAGCACAGATGAACAACAGAGACTGTCTGAATGTACAGAAC  
61 -----+-----+-----+-----+-----+-----+ 120  
GACGTCACGATAAGTACGTGTCGTCTACTTGTGTCTCTGACAGACTTACATGTCTTG  
L Q C Y S C T A Q M N N R D C L N V Q N -  
TGCAGCCTGGACCAGCACAGTTGCTTTACATCGCGCATCCGGGCCATTGGACTCGTGACA  
121 -----+-----+-----+-----+-----+-----+ 180  
ACGTCGGACCTGGTCGTGTCAACGAAATGTAGCGCGTAGGCCCGGTAACCTGAGCACTGT  
C S L D Q H S C F T S R I R A I G L V T -  
GTTATCAGTAAGGGCTGCAGCTCACAGTGTGAGGATGACTCGGAGAACTACTATTGCGC  
181 -----+-----+-----+-----+-----+-----+ 240  
CAATAGTCATTCCCGACGTCGAGTGTCACTCTACTGAGCCTCTTGATGATAAACCCG  
V I S K G C S S Q C E D D S E N Y Y L G -  
AAGAAGAACATCACGTGCTGCTACTCTGACCTGTGCAATGTCAACGGGGCCACACCCTG  
241 -----+-----+-----+-----+-----+-----+ 300  
TTCTTCTTGTAGTGACGACGATGAGACTGGACACGTTACAGTTGCCCCGGGTGTGGGAC  
K K N I T C C Y S D L C N V N G A H T L -  
AAGCCACCCACCACCCTGGGGCTGCTGACCGTGTCTGACGCTGTTGCTGTGGGGCTCC  
301 -----+-----+-----+-----+-----+-----+ 360  
TTCGGTGGGTGGTGGGACCCCGACGACTGGCACGAGACGTGGGACAACGACACCCCGAGG  
K P P T T L G L L T V L C S L L L W G S -  
AGCCGTCTGTAGGCTCTGGGAGAGCCTACCATAGCCCGATTGTGAAGGGATGAGCTGCAC  
361 -----+-----+-----+-----+-----+-----+ 420  
TCGGCAGACATCCGAGACCCTCTCGGATGGTATCGGGCTAACACTTCCCTACTCGACGTG  
S R L \*  
TCCACCCACCCCCACACAGG  
421 -----+-----+-----+-----+-----+ 441  
AGGTGGGGTGGGGGTGTGTCC

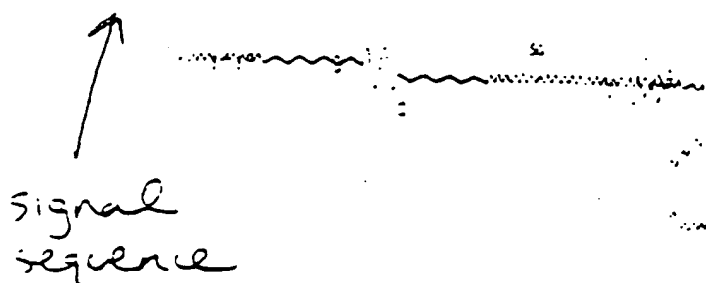
050700 " 03000000

1 MKIFLPVLLAALLGVERASS hSCA-2  
 1 MKA VLLAALLMAGLAALOPGTA hPSCA  
 1 MKT VLLAALLAATYLAALHPGAA mPSCA  
  
 21 LMCFSSCLNQKSNLYCEKPTI  
 21 LLCYSCKAQVSNEDCLQVEN\*  
 21 LQCYSCCTAQMNNRDCLNVQN\*  
  
 41 CSDDQDN YCVTVSASAGIGNL  
 41 CTQLGEGQCWTAIRAVGLLT  
 41 CSLDQHSCFTSRIRAI GLVT  
  
 61 VTFGHSLSKTCS PACPIPEG  
 61 V-----ISKGC SLN CVDDSQ  
 61 V-----ISKGCSS QCEDDSE  
  
 81 VNVGVASMGISCCQSFLCN\*F  
 76 DYYVGKK-N\*ITCCDIDL CN\*A  
 76 NYYLGKK-N\*ITCCYSDDL CN\*V  
  
 101 SAAADGG LRASVTLTGAGL L  
 95 SGNHAALOPAAAALLALPAAG  
 95 NGAHTLKPPTTLGLLTVLCS  
  
 121 SLTPALLRFGP  
 115 LLLWGPGL--  
 115 LLLWGS SRL--

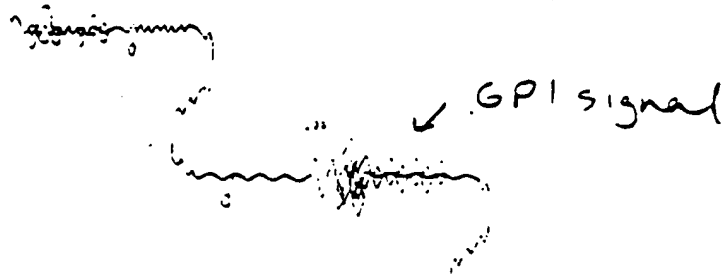
05030201.034000

FIG. 4



[illegible]

□ = glycosylation site



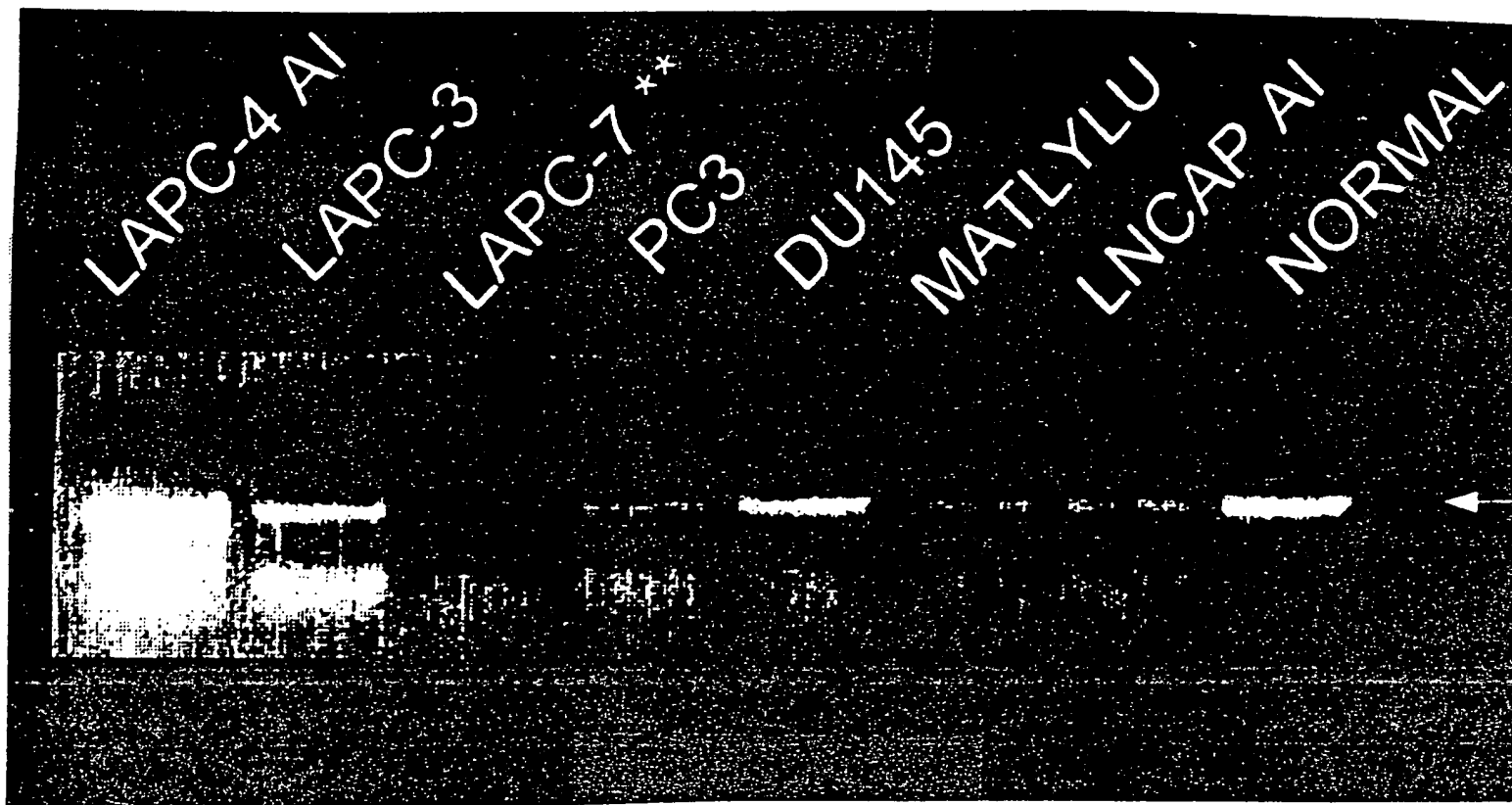
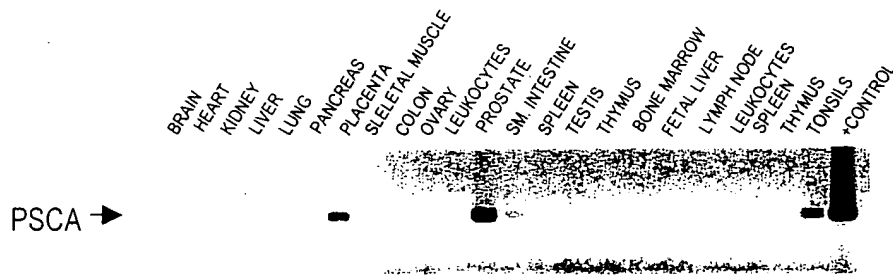
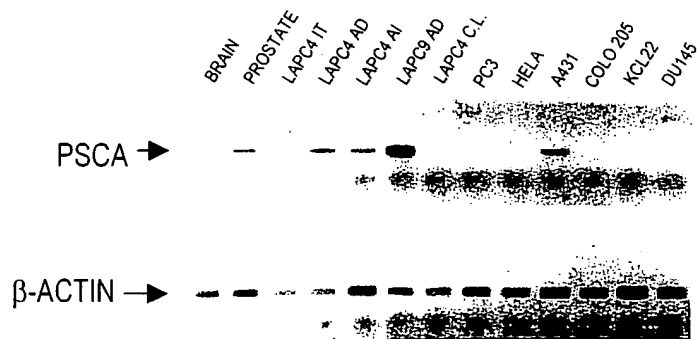


FIG. 7

A



B



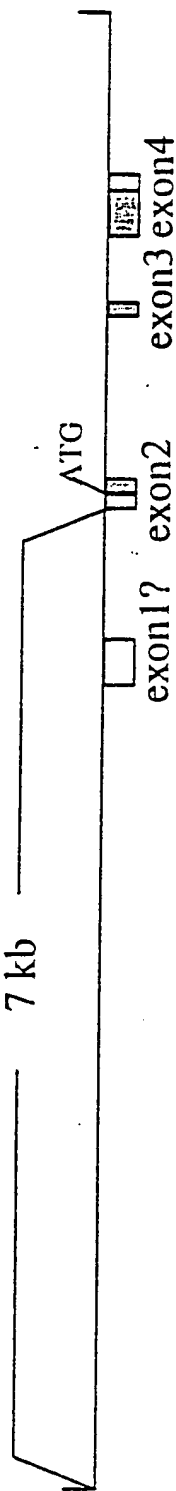
050338264 0340560



A. Ly-6/Thy-1 gene



B. mouse PSCA genomic clone (9 kb)



C. human PSCA genomic clone (14 kb)

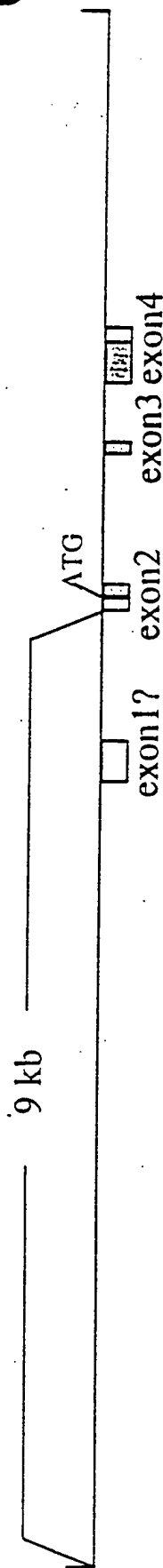


FIG. 15.

1G8

GST-PSCA  
GST-N-Terminal  
GST-Middle  
GST-C-Terminal



3E6

GST-PSCA  
GST-N-Terminal  
GST-Middle  
GST-C-Terminal



09030204.031099

FIG. 14.

950760 1929060

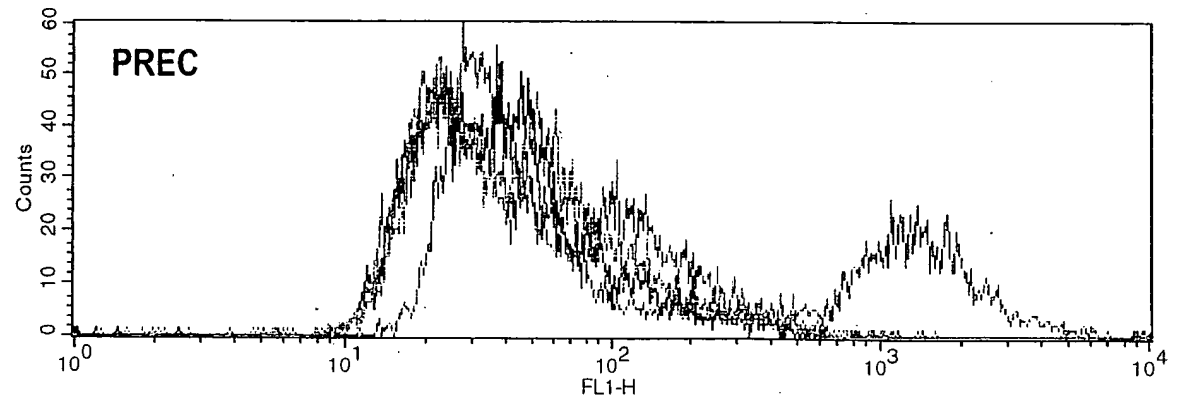
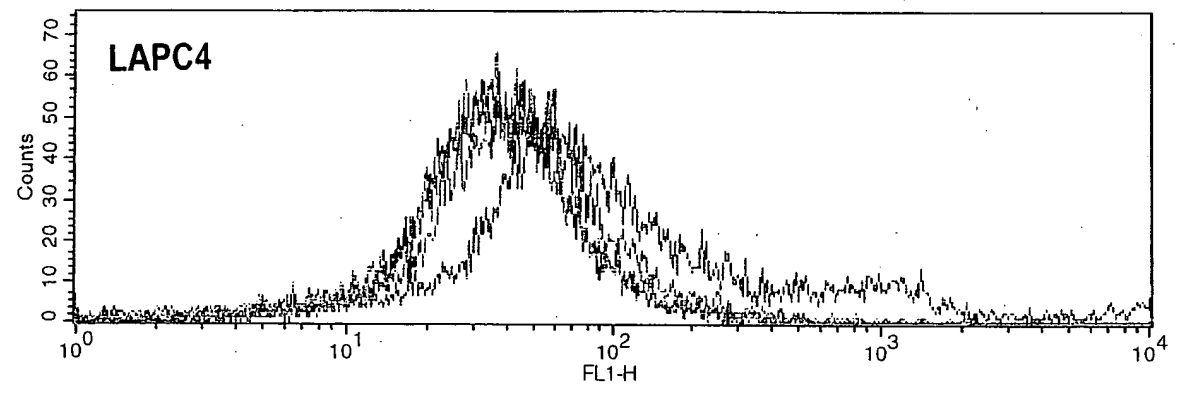
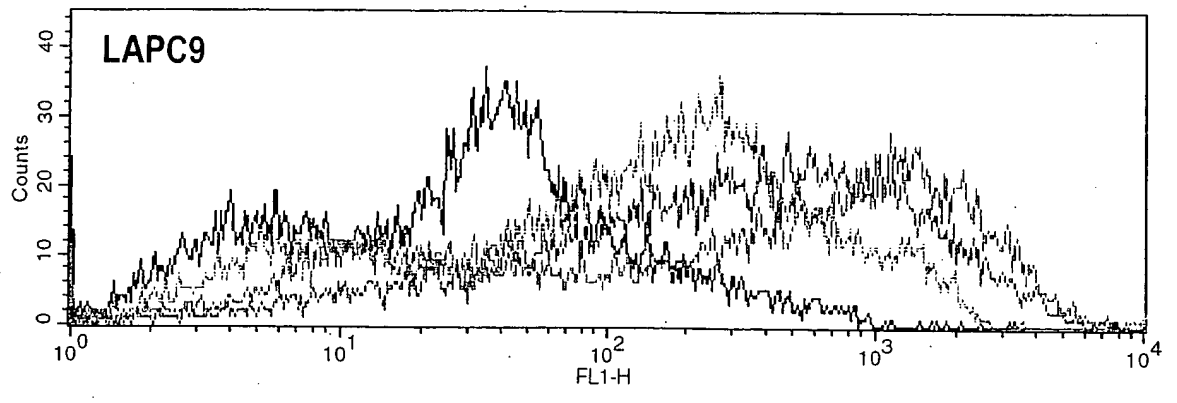
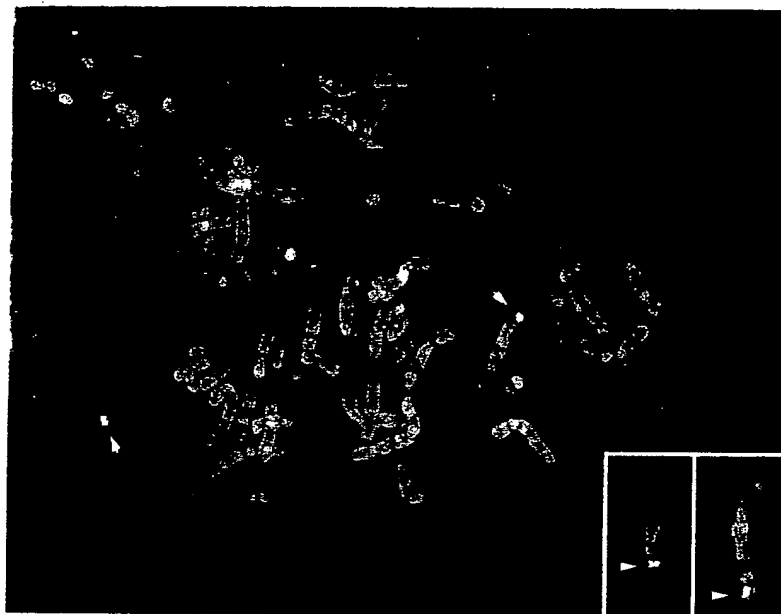


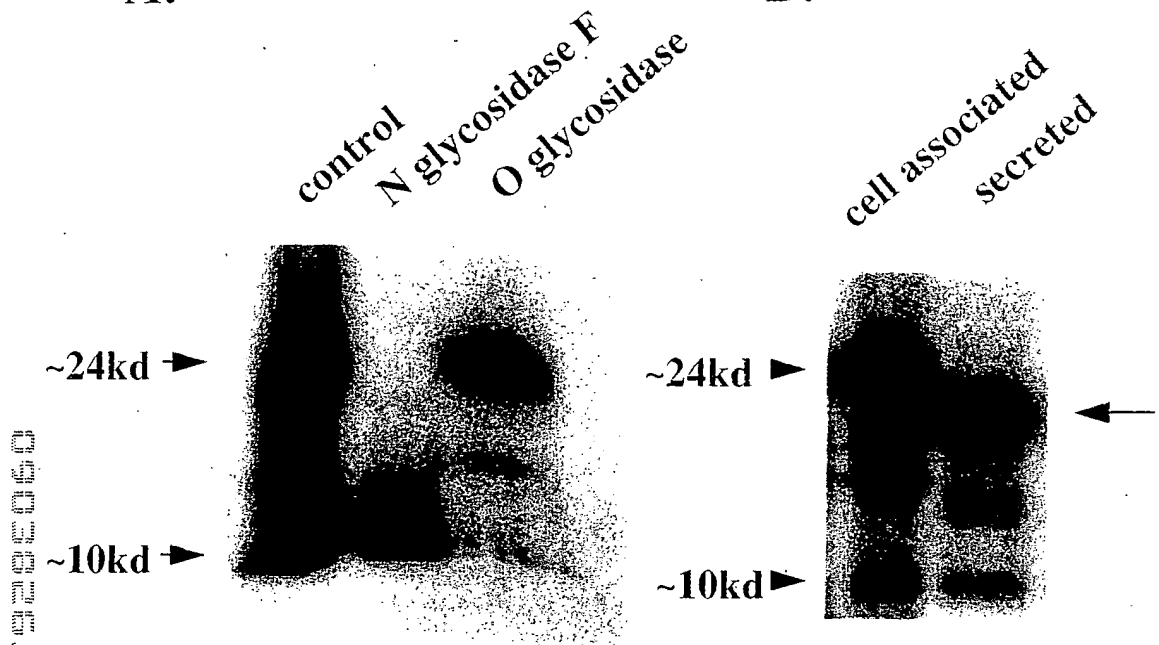
FIG. 13



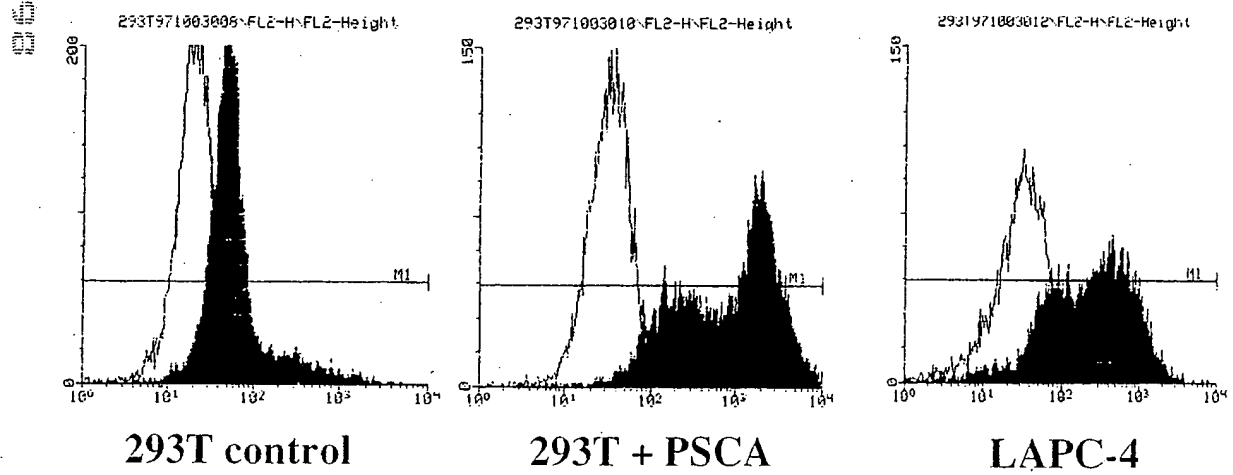
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A.

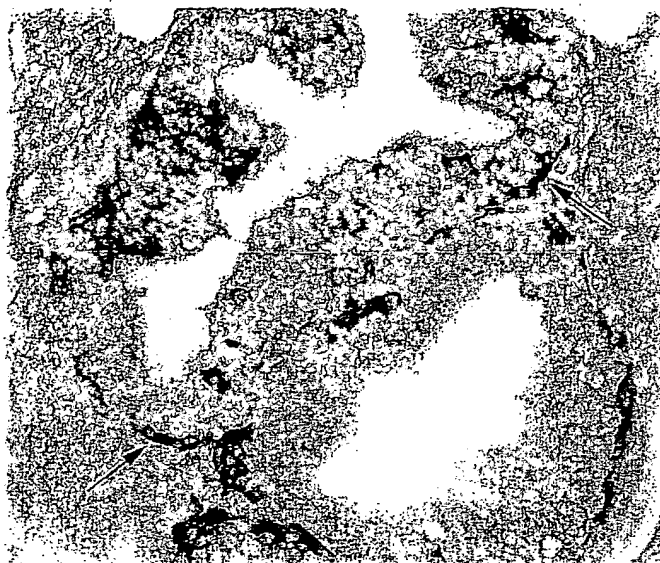
B.



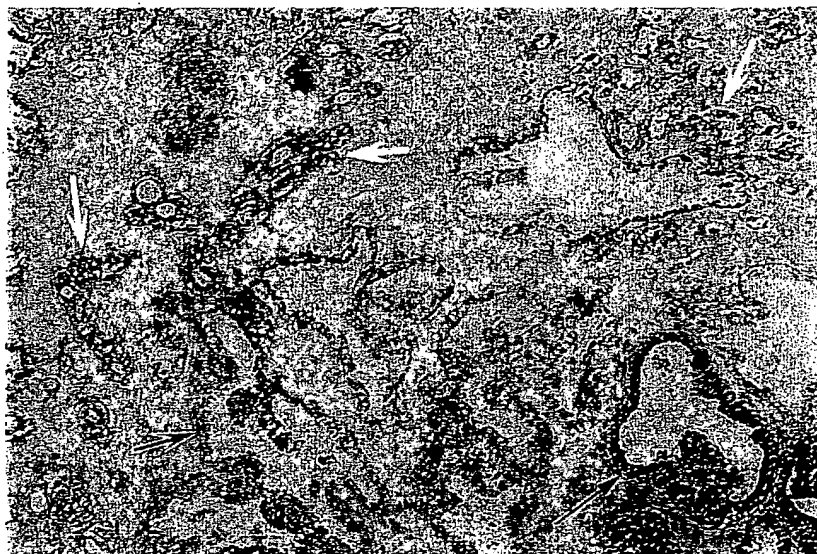
C.



A.



B.



C.



09038261.031058

*[The page contains faint, illegible markings or bleed-through from the reverse side.]*

72 HRS

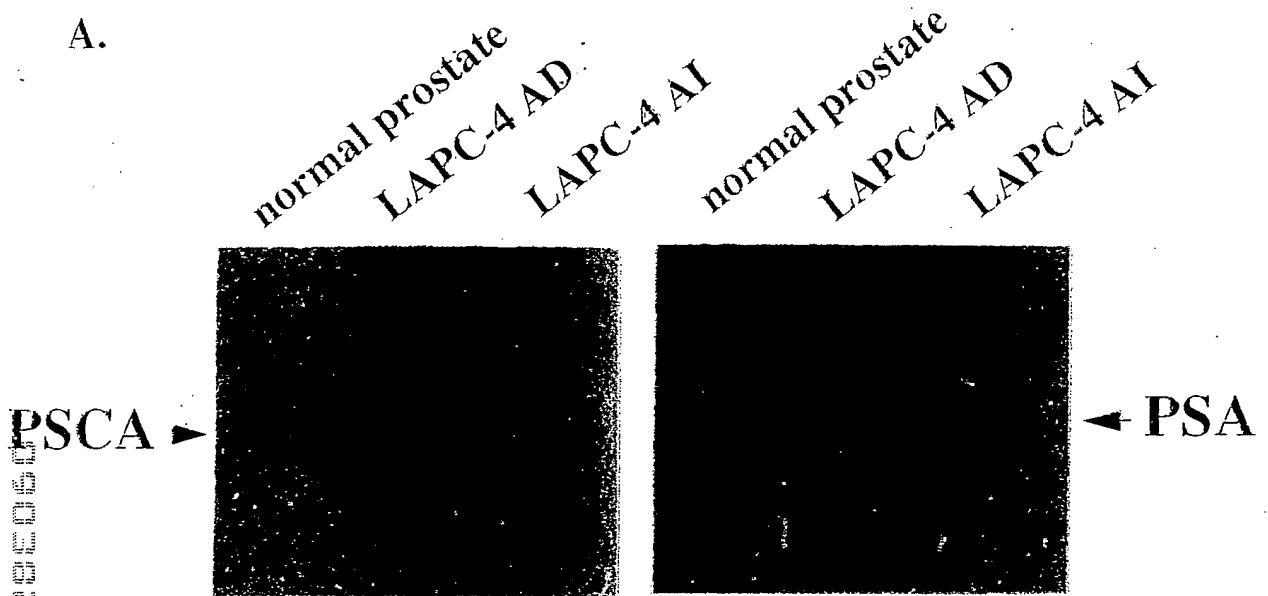
8PH  
LAPC4 AD  
LAPC4 AI  
LAPC4 IT  
LAPC9  
LAPC3 AI  
LAPC4 C.L.  
LNCAP  
PC3  
DU145  
HELA  
A431  
COLO 205  
KCL22

BPH  
LAPC4 AD  
LAPC4 AI  
LAPC4 IT  
LAPC9  
LAPC3 AI  
LAPC4 C.L.  
LNCAP  
PC3  
DU145  
HELA  
A431  
COLO 205  
KCL22

BPH  
LAPC4 AD  
LAPC4 AI  
LAPC4 IT  
LAPC9  
LAPC3 AI  
LAPC4 C.L.  
LNCAP  
PC3  
DU145  
HELA  
A431  
COLO 205  
KCL22

FIG. 9

A.



B.

